



COPY OF PAPERS
ORIGINALLY FILED

#4

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana

<120> 58860, A HUMAN CHOLESTERYL ESTER
HYDROLASE AND USES THEREFOR

<130> MPI2001-026P1RNM

<140> 10/056,744

<141> 2002-01-25

<150> 60/264,167

<151> 2001-01-25

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1325

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (16)...(1212)

<400> 1

```
taactaggca tttct atg atg tgg ctg ctt tta aca aca act tgt ttg atc 51
          Met Met Trp Leu Leu Leu Thr Thr Thr Cys Leu Ile
              1              5              10

tgt gga act tta aat gct ggt gga ttc ctt gat ttg gaa aat gaa gtg 99
Cys Gly Thr Leu Asn Ala Gly Gly Phe Leu Asp Leu Glu Asn Glu Val
          15              20              25

aat cct gag gtg tgg atg aat act agt gaa atc atc atc tac aat ggc 147
Asn Pro Glu Val Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly
          30              35              40

tac ccc agt gaa gag tat gaa gtc acc act gaa gat ggg tat ata ctc 195
Tyr Pro Ser Glu Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu
          45              50              55              60

ctt gtc aac aga att cct tat ggg cga aca cat gct agg agc aca ggt 243
Leu Val Asn Arg Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly
              65              70              75

ccc cgg cca gtt gtg tat atg cag cat gcc ctg ttt gca gac aat gcc 291
Pro Arg Pro Val Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala
              80              85              90

tac tgg ctt gag aat tat gct aat gga agc ctt gga ttc ctt cta gca 339
Tyr Trp Leu Glu Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala
          95              100              105

gat gca ggt tat gat gta tgg atg gga aac agt cgg gga aac act tgg 387
```

Asp	Ala	Gly	Tyr	Asp	Val	Trp	Met	Gly	Asn	Ser	Arg	Gly	Asn	Thr	Trp		
110						115					120						
tca	aga	aga	cac	aaa	aca	ctc	tca	gag	aca	gat	gag	aaa	ttc	tgg	gcc	435	
Ser	Arg	Arg	His	Lys	Thr	Leu	Ser	Glu	Thr	Asp	Glu	Lys	Phe	Trp	Ala		
125					130					135					140		
ttt	agt	ttt	gat	gaa	atg	gcc	aaa	tat	gat	ctc	cca	gga	gta	ata	gac	483	
Phe	Ser	Phe	Asp	Glu	Met	Ala	Lys	Tyr	Asp	Leu	Pro	Gly	Val	Ile	Asp		
				145					150					155			
ttc	att	gta	aat	aaa	act	ggg	cag	gag	aaa	ttg	tat	ttc	att	gga	cat	531	
Phe	Ile	Val	Asn	Lys	Thr	Gly	Gln	Glu	Lys	Leu	Tyr	Phe	Ile	Gly	His		
			160					165					170				
tca	ctt	ggc	act	aca	ata	ggg	ttt	gta	gcc	ttt	tcc	acc	atg	cct	gaa	579	
Ser	Leu	Gly	Thr	Thr	Ile	Gly	Phe	Val	Ala	Phe	Ser	Thr	Met	Pro	Glu		
		175					180					185					
ctg	gca	caa	aga	atc	aaa	atg	aat	ttt	gcc	ttg	ggg	cct	acg	atc	tca	627	
Leu	Ala	Gln	Arg	Ile	Lys	Met	Asn	Phe	Ala	Leu	Gly	Pro	Thr	Ile	Ser		
	190					195					200						
ttc	aaa	tat	ccc	acg	ggc	att	ttt	acc	agg	ttt	ttt	cta	ctt	cca	aat	675	
Phe	Lys	Tyr	Pro	Thr	Gly	Ile	Phe	Thr	Arg	Phe	Phe	Leu	Leu	Pro	Asn		
205					210					215					220		
tcc	ata	atc	aag	gct	gtt	ttt	ggg	acc	aaa	ggg	ttc	ttt	tta	gaa	gat	723	
Ser	Ile	Ile	Lys	Ala	Val	Phe	Gly	Thr	Lys	Gly	Phe	Phe	Leu	Glu	Asp		
				225					230					235			
aag	aaa	acg	aag	ata	gct	tct	acc	aaa	atc	tgc	aac	aat	aag	ata	ctc	771	
Lys	Lys	Thr	Lys	Ile	Ala	Ser	Thr	Lys	Ile	Cys	Asn	Asn	Lys	Ile	Leu		
			240					245					250				
tgg	ttg	ata	tgt	agc	gaa	ttt	atg	tcc	tta	tgg	gct	gga	tcc	aac	aag	819	
Trp	Leu	Ile	Cys	Ser	Glu	Phe	Met	Ser	Leu	Trp	Ala	Gly	Ser	Asn	Lys		
		255					260					265					
aaa	aat	atg	aat	cag	agt	cga	atg	gat	gtg	tat	atg	tca	cat	gct	ccc	867	
Lys	Asn	Met	Asn	Gln	Ser	Arg	Met	Asp	Val	Tyr	Met	Ser	His	Ala	Pro		
	270					275					280						
act	ggg	tca	tca	gta	cac	aac	att	ctg	cat	ata	aaa	cag	ctt	tac	cac	915	
Thr	Gly	Ser	Ser	Val	His	Asn	Ile	Leu	His	Ile	Lys	Gln	Leu	Tyr	His		
					290					295					300		
tct	gat	gaa	ttc	aga	gct	tat	gac	tgg	gga	aat	gac	gct	gat	aat	atg	963	
Ser	Asp	Glu	Phe	Arg	Ala	Tyr	Asp	Trp	Gly	Asn	Asp	Ala	Asp	Asn	Met		
				305					310					315			
aaa	cat	tac	aat	cag	agt	cat	ccc	cct	ata	tat	gac	ctg	act	gcc	atg	1011	
Lys	His	Tyr	Asn	Gln	Ser	His	Pro	Pro	Ile	Tyr	Asp	Leu	Thr	Ala	Met		
			320					325					330				
aaa	gtg	cct	act	gct	att	tgg	gct	ggg	gga	cat	gat	gtc	ctc	gta	aca	1059	
Lys	Val	Pro	Thr	Ala	Ile	Trp	Ala	Gly	Gly	His	Asp	Val	Leu	Val	Thr		
		335					340					345					
ccc	cag	gat	gtg	gcc	agg	ata	ctc	cct	caa	atc	aag	agt	ctt	cat	tac	1107	
Pro	Gln	Asp	Val	Ala	Arg	Ile	Leu	Pro	Gln	Ile	Lys	Ser	Leu	His	Tyr		

350		355		360	
ttt aag cta ttg cca gat tgg aac cac ttt gat ttt gtc tgg ggc ctc					1155
Phe Lys Leu Leu Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu					
365		370		375	380
gat gcc cct caa cgg atg tac agt gaa atc ata gct tta atg aag gca					1203
Asp Ala Pro Gln Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala					
	385		390		395
tat tcc taa atggaaaaaa aaaaaaaaaa aaaaaaaaaa aaagcggccg					1252
Tyr Ser *					
ctgaattcta gacctgccccg ggcggccgct cgagccctat agtgagtaag ggcgaattcg					1312
cggccgctaa att					1325
<210> 2					
<211> 398					
<212> PRT					
<213> Homo sapiens					
<400> 2					
Met Met Trp Leu Leu Leu Thr Thr Thr Cys Leu Ile Cys Gly Thr Leu					
1 5 10 15					
Asn Ala Gly Gly Phe Leu Asp Leu Glu Asn Glu Val Asn Pro Glu Val					
20 25 30					
Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly Tyr Pro Ser Glu					
35 40 45					
Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu Val Asn Arg					
50 55 60					
Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly Pro Arg Pro Val					
65 70 75 80					
Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala Tyr Trp Leu Glu					
85 90 95					
Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala Asp Ala Gly Tyr					
100 105 110					
Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Arg His					
115 120 125					
Lys Thr Leu Ser Glu Thr Asp Glu Lys Phe Trp Ala Phe Ser Phe Asp					
130 135 140					
Glu Met Ala Lys Tyr Asp Leu Pro Gly Val Ile Asp Phe Ile Val Asn					
145 150 155 160					
Lys Thr Gly Gln Glu Lys Leu Tyr Phe Ile Gly His Ser Leu Gly Thr					
165 170 175					
Thr Ile Gly Phe Val Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Arg					
180 185 190					
Ile Lys Met Asn Phe Ala Leu Gly Pro Thr Ile Ser Phe Lys Tyr Pro					
195 200 205					
Thr Gly Ile Phe Thr Arg Phe Phe Leu Leu Pro Asn Ser Ile Ile Lys					
210 215 220					
Ala Val Phe Gly Thr Lys Gly Phe Phe Leu Glu Asp Lys Lys Thr Lys					
225 230 235 240					
Ile Ala Ser Thr Lys Ile Cys Asn Asn Lys Ile Leu Trp Leu Ile Cys					
245 250 255					
Ser Glu Phe Met Ser Leu Trp Ala Gly Ser Asn Lys Lys Asn Met Asn					
260 265 270					
Gln Ser Arg Met Asp Val Tyr Met Ser His Ala Pro Thr Gly Ser Ser					
275 280 285					
Val His Asn Ile Leu His Ile Lys Gln Leu Tyr His Ser Asp Glu Phe					
290 295 300					
Arg Ala Tyr Asp Trp Gly Asn Asp Ala Asp Asn Met Lys His Tyr Asn					

305		310		315		320
Gln Ser His Pro Pro	Ile Tyr Asp Leu Thr	Ala Met Lys Val Pro Thr				
	325	330		335		
Ala Ile Trp Ala Gly Gly	His Asp Val Leu Val Thr	Pro Gln Asp Val				
	340	345		350		
Ala Arg Ile Leu Pro Gln	Ile Lys Ser Leu His Tyr	Phe Lys Leu Leu				
	355	360		365		
Pro Asp Trp Asn His Phe	Asp Phe Val Trp Gly	Leu Asp Ala Pro Gln				
	370	375		380		
Arg Met Tyr Ser Glu Ile	Ile Ala Leu Met Lys	Ala Tyr Ser				
385	390	395				

<210> 3
 <211> 1194
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1194)

<400> 3															
atg atg tgg ctg ctt tta aca aca act tgt ttg atc tgt gga act tta	48														
Met Met Trp Leu Leu Leu Thr Thr Thr Cys Leu Ile Cys Gly Thr Leu															
1 5 10 15															
aat gct ggt gga ttc ctt gat ttg gaa aat gaa gtg aat cct gag gtg 96															
Asn Ala Gly Gly Phe Leu Asp Leu Glu Asn Glu Val Asn Pro Glu Val															
20 25 30															
tgg atg aat act agt gaa atc atc atc tac aat ggc tac ccc agt gaa 144															
Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly Tyr Pro Ser Glu															
35 40 45															
gag tat gaa gtc acc act gaa gat ggg tat ata ctc ctt gtc aac aga 192															
Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu Leu Val Asn Arg															
50 55 60															
att cct tat ggg cga aca cat gct agg agc aca ggt ccc cgg cca gtt 240															
Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly Pro Arg Pro Val															
65 70 75 80															
gtg tat atg cag cat gcc ctg ttt gca gac aat gcc tac tgg ctt gag 288															
Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala Tyr Trp Leu Glu															
85 90 95															
aat tat gct aat gga agc ctt gga ttc ctt cta gca gat gca ggt tat 336															
Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala Asp Ala Gly Tyr															
100 105 110															
gat gta tgg atg gga aac agt cgg gga aac act tgg tca aga aga cac 384															
Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Arg His															
115 120 125															
aaa aca ctc tca gag aca gat gag aaa ttc tgg gcc ttt agt ttt gat 432															
Lys Thr Leu Ser Glu Thr Asp Glu Lys Phe Trp Ala Phe Ser Phe Asp															
130 135 140															
gaa atg gcc aaa tat gat ctc cca gga gta ata gac ttc att gta aat 480															
Glu Met Ala Lys Tyr Asp Leu Pro Gly Val Ile Asp Phe Ile Val Asn															
145 150 155 160															

aaa act ggt cag gag aaa ttg tat ttc att gga cat tca ctt ggc act	528
Lys Thr Gly Gln Glu Lys Leu Tyr Phe Ile Gly His Ser Leu Gly Thr	
165 170 175	
aca ata ggg ttt gta gcc ttt tcc acc atg cct gaa ctg gca caa aga	576
Thr Ile Gly Phe Val Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Arg	
180 185 190	
atc aaa atg aat ttt gcc ttg ggt cct acg atc tca ttc aaa tat ccc	624
Ile Lys Met Asn Phe Ala Leu Gly Pro Thr Ile Ser Phe Lys Tyr Pro	
195 200 205	
acg ggc att ttt acc agg ttt ttt cta ctt cca aat tcc ata atc aag	672
Thr Gly Ile Phe Thr Arg Phe Phe Leu Leu Pro Asn Ser Ile Ile Lys	
210 215 220	
gct gtt ttt ggt acc aaa ggt ttc ttt tta gaa gat aag aaa acg aag	720
Ala Val Phe Gly Thr Lys Gly Phe Phe Leu Glu Asp Lys Lys Thr Lys	
225 230 235 240	
ata gct tct acc aaa atc tgc aac aat aag ata ctc tgg ttg ata tgt	768
Ile Ala Ser Thr Lys Ile Cys Asn Asn Lys Ile Leu Trp Leu Ile Cys	
245 250 255	
agc gaa ttt atg tcc tta tgg gct gga tcc aac aag aaa aat atg aat	816
Ser Glu Phe Met Ser Leu Trp Ala Gly Ser Asn Lys Lys Asn Met Asn	
260 265 270	
cag agt cga atg gat gtg tat atg tca cat gct ccc act ggt tca tca	864
Gln Ser Arg Met Asp Val Tyr Met Ser His Ala Pro Thr Gly Ser Ser	
275 280 285	
gta cac aac att ctg cat ata aaa cag ctt tac cac tct gat gaa ttc	912
Val His Asn Ile Leu His Ile Lys Gln Leu Tyr His Ser Asp Glu Phe	
290 295 300	
aga gct tat gac tgg gga aat gac gct gat aat atg aaa cat tac aat	960
Arg Ala Tyr Asp Trp Gly Asn Asp Ala Asp Asn Met Lys His Tyr Asn	
305 310 315 320	
cag agt cat ccc cct ata tat gac ctg act gcc atg aaa gtg cct act	1008
Gln Ser His Pro Pro Ile Tyr Asp Leu Thr Ala Met Lys Val Pro Thr	
325 330 335	
gct att tgg gct ggt gga cat gat gtc ctc gta aca ccc cag gat gtg	1056
Ala Ile Trp Ala Gly Gly His Asp Val Leu Val Thr Pro Gln Asp Val	
340 345 350	
gcc agg ata ctc cct caa atc aag agt ctt cat tac ttt aag cta ttg	1104
Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr Phe Lys Leu Leu	
355 360 365	
cca gat tgg aac cac ttt gat ttt gtc tgg ggc ctc gat gcc cct caa	1152
Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu Asp Ala Pro Gln	
370 375 380	
cgg atg tac agt gaa atc ata gct tta atg aag gca tat tcc	1194
Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala Tyr Ser	
385 390 395	

<210> 4
 <211> 233
 <212> PRT
 <213> Homo sapiens

<400> 4
 Phe Arg Val Ile Ala Leu Asp Leu Arg Gly Phe Gly Glu Ser Ser Arg
 1 5 10 15
 Pro Ser Asp Leu Ala Asp Tyr Arg Phe Asp Asp Leu Ala Glu Asp Leu
 20 25 30
 Glu Ala Leu Leu Asp Ala Leu Gly Leu Asp Lys Pro Val Ile Leu Val
 35 40 45
 Gly His Ser Met Gly Gly Ala Leu Ala Ala Tyr Ala Ala Lys Tyr
 50 55 60
 Pro Glu Glu Arg Val Lys Ala Leu Val Leu Val Ser Thr Pro Ala Pro
 65 70 75 80
 Ala Gly Leu Ser Ser Arg Leu Phe Pro Arg Leu Gly Asn Leu Glu Gly
 85 90 95
 Leu Leu Leu Ala Asn Phe Phe Asn Arg Leu Ser Arg Ser Val Glu Ala
 100 105 110
 Leu Leu Gly Arg Ala Leu Lys Gln Phe Phe Leu Leu Gly Arg Pro Phe
 115 120 125
 Val Ser Asp Phe Leu Lys Gln Ala Glu Asp Trp Leu Ser Ser Leu Ala
 130 135 140
 Arg Pro Gly Glu Thr Asp Gly Gly Asp Gly Leu Leu Gly Tyr Ala Val
 145 150 155 160
 Ala Leu Gly Lys Leu Leu Gln Trp Asp Arg Ser Ala Leu Lys Asp Ile
 165 170 175
 Lys Val Pro Thr Leu Val Ile Trp Gly Asp Asp Asp Pro Leu Val Pro
 180 185 190
 Leu Lys Ala Ser Glu Lys Leu Ser Ala Leu Phe Pro Asn Ala Glu Val
 195 200 205
 Val Val Ile Asp Asp Ala Gly His Leu Ala Leu Leu Glu Lys Pro Glu
 210 215 220
 Glu Val Ala Glu Leu Ile Lys Phe Leu
 225 230

<210> 5
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 5
 Trp Ile Ala Asn Gly Pro Asn Lys Ser Leu Ala Phe Ile Leu Ala Asp
 1 5 10 15
 Ala Gly Tyr Asp Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Tyr Ser
 20 25 30
 Arg Lys His Val Lys Leu Asn Pro Ser His Ser Glu Phe Trp Asp Phe
 35 40 45
 Ser Trp His Glu Met Gly Met Tyr Asp Leu Pro Ala Met Ile Asp Tyr
 50 55 60
 Val Leu Glu Thr Thr Gly Gln Glu Lys Leu His Tyr Val Gly His Ser
 65 70 75 80
 Gln Gly Thr Thr Val Phe Phe Val Met Leu Ser Glu Arg Pro Glu Tyr
 85 90 95
 Asn Glu Lys Ile Lys Ser Phe His Ala Leu Ala Pro Val Ala Tyr Met
 100 105 110
 Lys His Val Arg Ser Pro Leu Val Lys Leu Leu Ala Pro Gln Ser

<210> 6

<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(1)
<223> Xaa = L, I or V

<223> The amino acid at position 2 can be any amino acid

<221> VARIANT
<222> (3)...(3)
<223> Xaa = L, I, V, M, S or T

<221> VARIANT
<222> (4)...(4)
<223> Xaa = L, I, V, M, S or T

<221> VARIANT
<222> (6)...(6)
<223> Xaa = H, Y, W or V

<223> The amino acid at position 8
can be any amino acid

<221> VARIANT
<222> (10)...(10)
<223> Xaa = G, T, A or C

<400> 6
Xaa Xaa Xaa Xaa Gly Xaa Ser Xaa Gly Xaa
1 5 10